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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat May 13 08:27:01 2000; MasPar time 19.30 Seconds 644.282 Million cell updates/sec

Description:
Perfect Score:
Sequence:

>US-09-331-631-7
(1-525) from US09331631.pep (1 of 3)
3808
1 MVISKSPFIVLIFSLLLSFA.....FLNHKQNTNVIKFTVKASAY 525

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 35.694; Variance 169.035; scale 0.211

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

23	21	20	19	18	17	16	15	14	13	12	11	10	9	ω	7	0	υ	4	ω	2	_	Result No.
133	133	133	146	147	169	593	680	702	724	729	752	796	796	810	848	1149	1178	1193	1910	3654	3808	Score
ω ω  	ω 	3. 5	3.8	3.9	4.4	15.6	17.9	18.4	19.0	19.1	19.7	20.9	20.9	21.3	22.3	30.2	30.9	31.3	50.2	96.0	100.0	Query Match
94	86	86	521	186	395	637	444	524	409	489	626	614	614	605	593	625	666	666	590	566	525	Query Match Length
р р	<u>_</u>	ш	μ	Н	<u> </u>	ب	<u>_</u>	ب	نسا	<b></b> .	$\vdash$	۳,	ш	<u>, , , , , , , , , , , , , , , , , , , </u>	Н	Ъ	بر	ب	۳	$\vdash$	щ	BG
W95080 W95075	W95078	W95073	W74802	W26536	W03474	W62837	W90340	W90339	W90342	W90341	W22150	W62834	W22149	W62838	W62835	W62830	W62828	W62829	W62832	R20181	W62831	ID
GST-HD fusion protein GST-HD fusion protein	fusion	GST-HD fusion protein	Human secreted protein	Trypanosoma cruzi anti	Mouse SRY-related prot	Hordeum vulgare antimi	G. max truncated SBP1	. max	max	G. max SBP2 protein.	Peanut allergen Ara hI	Arachis hypogaea antim	Peanut allergen Ara hI	Glycine max antimicrob	Zea mays antimicrobial	Macadamia integrifolia	Macadamia integrifolia	Macadamia integrifolia	Gossypium hirsutum ant	Sequence encoded by 67	Theobroma cacao antimi	Description
2.26e-01 2.26e-01	2.26e-01	. 26e	2.61e-02		5.11e-04	2.12e-39	5.41e-47	6.39e-49	7.49e-51	2.73e-51	2.59e-53	3.46e-57	.46e-5	.02e-5	8.89e-62	1.60e-88	4.11e-91	1.88e-92	7.10e-157	0.00e+00	0.00e+00	Pred. No.

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301 KLEEILEEQRGQKRQQGQQGMFRKAKPEQIRAISQQATSPRHRGGERLAINLLSQSPVYS 360

45	44	<b>4</b> 3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
112	115	115	115	113	115	116	115	118	118	117	123	123	121	122	121	120	120	120	121	131	130
2.9	3.0		3.0		3.0			3.1		3.1	•	3.2									3.4
96	499	386	386	96	96	96	69	539	96	28	1311	1311	432	428	371	303	108	108	96	567	562
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W99832	P82755	R06849	R04828	W99837	W99833	W99830	R13399	W33628	W99836	W62841	W52197	W72971	W93954	R85851	W73369	R60054	W95076	W95071	W99838	W88788	R70491
HIV A30S protein seque	Rice storage protein.	Protein Arp 4.		HIV G75A protein seque	HIV A30L protein seque	HIV Vpr protein sequen	Protein contg. IgA bin	Yeast transcriptional	HIV H71C protein seque	Stenocarpus sinuatus a	Precis coenia (butterf	Precis coenia patched	Human regulatory molec	WD-40 domain-contg. AA	Epitope tagged TBP pro	Dirofilaria immitis pa	Amino acid sequence of	Amino acid sequence of	HIV C76S protein seque	Polypeptide fragment e	Leucocytozoan protozoa
6.53e+00	4.08e+00	4.08e+00	4.08e+00	5.58e+00	4.08e+00	3.49e+00	4.08e+00	2.54e+00	2.54e+00	2.98e+00	1.15e+00	1.15e+00	1.58e+00	1.34e+00	1.58e+00	1.85e+00	1.85e+00	1.85e+00	1.58e+00	3.14e-01	3.69e-01

## ALIGNMENTS

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241 TVYVVSQDNQEKLTIAVLALPVNSPGKYELFEPAGNNKPESYYGAFSYEVLETVFNTQRE 300	N	Qy
241 TVYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAFSYEVLETVFNTQRE 300		ďď
181 DYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVORGTVVSVPAGS 240		QΨ
181 DYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGS 240		ďď
121 HENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGIN 180		QΥ
121 HENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGIN 180		ф
61 QCEQRCEREYKEQQRQQEEELQRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGE 120		Qγ
61 QCEQRCEREYKEQQRQQEEELQRQYQQCQGRCQEQQQQGQREQQQCQRKCWEQYKEQERGE 120		Дd
1 MVISKSPFIVLIFSLLLSFALLCSGVSAYGRKQYERDPRQQYEQCQRRCESEATEEREQE 60		Qy
1 MVISKSPFIVLIFSLLLSFALLCSGVSAYGRKQYERDPRQQYEQCQRRCESEATEEREQE 60		В
Query Match 100.0%; Score 3808; DB 1; Length 525; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query M Best Lo Matches	
Sequence 525 AA;		SC
be used to control micropial infestations in plants and mammalian animals.		9 8
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Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals		T'q
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ROWER NT. GOUTER KC. Green JL. Manners JM. Marcus JP:		י ט בי בי
AU-004275.		PR
DEC-1997;		ΡF
02-JUL-1998.		Ϋ́
Theoproma cacao.		PNG
antimicrobial protein; infestation; control.		KW
Theobroma cacao antimicrobial protein.		DE
27-OCT-1998 (first entry)		DI
W62831 standard; Protein; 525 AA.		S U
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant cocoa proteins - are responsible beans and produced in large quantities using expression vectors
Claim 4; Fig 2; 59pp; English.
The inventors claim a 67 kD and 31 kD T. caca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-1991. G00914. 07-JUN-1991; G00914. 11-JUN-1990; GB-013016. (MRSC ) MARS UK LTD. Spencer ME, Hodge R, Deakin EA, Ashton WPI; 92-024418/03. N-PSDB; Q20377.
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be encoded by 67 kD T. of flavour; vicilin; seed
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10; Mismatches 6
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The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9827805-A1.
02-JUL-1998.
22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
CODER RES CENT TROPICAL PLANT PATHOLOGY.
BOWER NI, Goulter KC, Green JL, Manners JM, Marcus
WPI; 98-377279/32.
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                                                    RSRLSRGDIFVVPANFPVTFVASQNQNLRMTGFGLYNQN
                                                                                                        VPHYNSKATFVVFVTDGYGYADMACPHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQV
                                                                                                                                      VPHYNSKATFYILVTEGNGYAEMVSPHLPRQSSYEEEEEEEEDEEEEQQQEEERRSGQYRKI 491
                                                                                                                                                                                                                QATSPRHRGGERLAINLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIF
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261; Conser
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ilarity 56.9%;
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Pred. No. 7.10e-157;
95; Mismatches 92;
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plants or mar
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WPI: 98-377279/32.
N-PSDB: V43311.
Novel anti-mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                   Macadamia integrifolia antimicrobial antimicrobial protein; infestation; Macadamia integrifolia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel anti-microbial protein from e.g. Macadamia integrifo: useful for controlling microbial infestations of plants or Claim 1; Page 39-41; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and marketing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1998.
22-DEC-1997;
20-DEC-1996;
                                                        W62828;
27-OCT-1998 (first entry)
 Peptide
                                                                            W62828 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antimicrobial protein; infestation; c Macadamia integrifolia. Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                             AILLYTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTEYLINRDNNERLHIAKFLQTIS
                                                                                                                                                                                                                                                                                                                                                                                                                  YEDCRRRC-EQQE-PRQQYQCQRRCREQQRQHGRGGDLINPQRGGSGRYEEGEEKQSDNP
                                                                                                                           SEEETFGEFQQVKAPLSPGDVFVAPAGHAVTFFASKDQPLNAVAFGLNAQNNQRIFLAGR
                                                                                                                                                                    VSAFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQMACPHLSRQSQGSQGRQDRREQEEE
                                                                                                                                                                                 KAKPEQIRAISQQATSPRHRGGERLAINLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVA
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195; Conser
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(larity 40.6%;
Conservative
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29 .666
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Green JL, Manners JM, Marcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1193; DB 1;
Pred. No. 1.88e-92;
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IDENTIFICATION OF THE KW and K
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Best Local S
Matches 19
                  02-JUL-1998.
22-DEC-1997;
20-DEC-1996;
                                                                                                                                                                                                                                       W62830; standard; Protein; 625 AA. W62830; Cfirst entry)
27-OCT-1998 (first entry)
Macadamia integrifolia antimicrobial antimicrobial protein; infestation; c
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The sequence is that of an antimicrobial pe used to control microbial infestations animals.
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02-JUL-1998.
22-DEC-1997;
20-DEC-1996;
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Bower NI, Goulter KC,
WPI; 98-377279/32.
    (RETR-) COOP
                                                                                                                                      Protein
                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGSTVYVVSQDNQEKLTIAVLALPVNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDV--HYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQMACPHLSRQSQGSQSGRQDRREQEEESE 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRDD--SESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EETFGEFQQVKAPLSPGDVFVAPAGHAVTFFASKDQPLNAVAFGLNAQNNQRIFLAGR
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191; Conser
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ilarity 40.0%;
Conservative
AU0874.
AU-004275.
RES CENT TROPICAL
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AU-004275.
                                                                                                            /note= "signal
29. .666
/note= "mature
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29. .66
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Pred. No. 4.11e-91;
125; Mismatches 139;
    PLANT PATHOLOGY
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Query Match
Best Local S
Matches 16
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Best Local S
Matches 19
                                                                             Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals claim 1; Page 58-60; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian
                                                                                                                                             02-JUL-1998.
22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Bower NI, Goulter KC, Green JL, Manners JM, Maj
BOWER NI, GOULTER KC, Green JL, Manners JM, Maj
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The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mar
                                                         Sequence
                                                                         animals
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    Local Similarity nes 161; Conser
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mays antimicrobial pro
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:| |:|:: :::|:||||:: | |: :::|| |:| |: :::|
YFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGSTVYVVSQDNQEKLTIAVLALPVNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEV--HYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRDD--SESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVF 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCRRHC-EQQE-PRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGEEKQSDNPYY 212
                                                                                                                                                                                                                                                                                                                                                                      EETFGEFQQVKAPLSPGDVFVAPAGHAVTFFASKDQPLNAVAFGLNAQNNQRIFLAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                          IANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGR-HGGRGG--GKR-HEEE-- 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPEQIRAISQQATSPRHRGGERLAINLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVS
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larity 35.2%;
Conservative
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infestation; control
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     118;
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Pred. No. 1.60e-88;
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    Mismatches
                  848; DB 1;
No. 8.89e-62;
                                                                                                                                                                   Marcus
                             Length
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    29;
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Best Local S
Matches 16
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22-DEC-1997; AU0874.
22-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(REIR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Bower NI, Goulter KC, Green JL, Manners JM, Marcu
WPI; 98-377279/32
Novel anti-microbial protein from e.g. Macadamia
useful for controlling microbial infestations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 63-65; 96pp; English.

The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max antimicrobial protein. antimicrobial protein; infestation;
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il Similarity 34.6%;
167; Conservatta
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Pred. No. 2.02e-58;
134; Mismatches 146
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                                                                                   Query Match
Best Local S
Matches 15
                                                                                                                                                                                                           reanut allergens Ara hI and Ara hII - used for vaccination and in two-site monoclonal antibody based ELISA.

S Claim 31; Page 169; 354pp; English.

C This polypeptide comprises major peanut allergen Ara hI (W22149).

C Its sequence was deduced from cDNA clone P17 (T76612), isolated from peanut seed cDNA using a primer (see T76616) based on an cisolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum C IgE from a large proportion of individuals with peanut chypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site binding Ara hI antigen epitopes (see W24165-87) may be used in conclines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock.
                                                                                                                                                                                             e.g. anap
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody; ELISA; analysis; Ara hI.
Arachis hypogaea strain Florunner.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-1997.
23-SEP-1996; U15222.
04-MAR-1996; US-610424.
29-DEC-1995; US-009455.
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Bannon GA, Burks AW,
WPI; 97-363453/33.
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Peanut allergen Ara hI.
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153; Conse
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Pred. No. 3.46e-57;
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22-DEC-1997;
20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants Claim 1; Page 55-57; 96pp; English.

The sequence is that of an antimicrobial protein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY Bower NI, Goulter KC, Green JL, Manners JM, Ma WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arachis hypogaea antimantimicrobial protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W62834 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9827805-A1.
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DNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAFSYEVLETVFNTQ-RE--K--L
                                                                                                                                        EARPNTLYLPKHADADNILYIQQGQATYTVANGNNRKSFNLDEGHALRIPSGFISYILNR 271
                                                                                                                                                                                                                                               GTPGSEVREETSRNNPFYFPSRR-FSTRYGNQNGRIRVLQRFDQRSKQFQNLQNHRIVQI 211
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                                                    HDNQNLRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLL 331
                                                                                                                                                                                                                                                                                                                     EYKEQQRQQEEELQRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGE-HENYHNH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGYGYAQMACPHLSRQSQGSQSGRQDRREQEEESEEETFG-EFQQVKAPLSPGDVFVAPA
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                                                                                                       EANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGSTVYVVSQ
                                                                                                                                                                                                                 KKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAMF
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153; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 3.46e-57,
126; Mismatches 150
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plants or man
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RESULTANT NEW PROPERTY OF STREET PROPERTY OF STREET
                                                                                                                                                                                                                                                                                                                                                                                      CC Its sequence was deduced from cDNA clone P41b (T76613), isolated cc from peanut seed cDNA using a primer (see T76616) based on an CC isolated Ara hI peptide (see W24206). The sequence shows consistivated homology with the vicilin family of seed storage cc proteins of other legumes. The allergen is recognised by serum cc IgE from a large proportion of individuals with peanut cc hypersensitivity. Ara hI and Ara hII (see W24164) can be used to craise monoclonal antibodies which are used in a specific two-site cc wach service and in a state of the consistivity. The detection of Ara hII or Ara hII (claimed). IgE-cc binding Ara hI antigen epitopes (see W24165-87) may be used in creg. anaphylactic shock.
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                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peanut allergens Ara hI and Ara hII - used for vaccination and
two-site monoclonal antibody based ELISA
Claim 31; Page 172; 354pp; English.
This polypeptide comprises major peanut allergen Ara hI (W22149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 97-363453/33.
N-PSDB; T76613.
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04-MAR-1996; US-610424.
29-DEC-1995; US-009455.
(UYAR-) UNIV ARKANSAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peanut; seed storage protein; allergen; aller vaccine; anaphylactic shock; immunotherapy; trono-lonal antibody; ELISA; analysis; Ara hI. Arachis hypogaea strain Florunner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-1997 (first entry)
Peanut allergen Ara hI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W22150;
29-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bannon GA,
218
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                                                                                                                                                                                                  DYDDDRRQPRREEGGRWGPAGPREREEEDWRQPREDWRRPSHQQPRKIRPEGREGEQEW 158
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EAKPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNR 277
                                                       KKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAMF
                                                                                     GTPGSHVREETSRNNPFYFPSRR-FSTRYGNQNGRIRVLQRFDQRSRQFQNLQNHRIVQI 217
                                                                                                                                                               EYKEQQRQQEEELQRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGE-HENYHNH 127
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                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burks AW, Cockrell G,
                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                    123;
                                                                                                                                                                                                                                                                                                            Score 752; DB 1;
Pred. No. 2.59e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergen; allergy; hypersensitivity;
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EEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAMFEANPN EQHEEEEDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEARAH 147

88

29 75

KETEVEEDPELVTCKHQCQQQRQYTESDKRTCLQQC-DSMKQEREKQVEEETREKEEEEHQ 87 :: | | : | : | : | : | : : :: ::

ROQEEELORQYQQCQGRCQEQQQ-GQREQQQCQRKCWEQYK-EQERGEHENYHNHKKNRS

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192

Local Similarity

Conservative

Mismatches 133;

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Query Match
Best Local (
                                                                                                                                                                                                                                                             This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as sybban). In contrast, decreased sucrose uptake activity in
                                                                                                                                    seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max. WO9853086-A1.
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seed; carbohydrate content; soybean.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uptake activity in developing seeds Claim 13b; Page 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chao WS, Grimes HD; WPI; 99-070155/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose
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(UNIW ) UNIV WASHINGTON
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                                                                                                        489 AA;
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Score 729; DB 1;
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The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
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                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                              transgene
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(UNIW ) UNIV WASHINGTON STATE RES FOUND.
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21-MAY-1998; U10465
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133
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max truncated SBP2 protein.
pl; sucrose binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFVSPRHFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDENEK 207
EEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAMFEANPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N--EG--SIFKISR-ERVRALAPTKKSSWWPFGGESKAQFNIFSKRPTFSNGYGRLTEVG
                                   EQHEEEEDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEARAH
                                                                         RQQEEELQRQYQQCQGRCQEQQQ-GQREQQQCQRKCWEQYK-EQERGEHENYHNHKKNRS 132
                                                                                                                 KETEVEEDPELVTCKHQCQQQRQYTESDKRTCLQQC-DSMKQEREKQVEEETREKEEEHQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNAQNNQRIFLAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEDFSQ-FQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQMACPHLSRQSQG
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                                                                                                                                                           118;
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                         in developing seeds.
                                                                                                                                                       19.0%;
larity 32.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503
                                                                                                                                                       Score 724; DB 1; Le pred. No. 7.49e-51; 114; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SBP2; sucrose uptake; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or decreased sucrose
                                                                                                                                                                                             Length 409
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130

NRSEEEEGQQ-

93 79

34 EEEDPELVTCKHQCQQQQQYTEGDKRVCLQSC-DRYHRMKQEREKQIQEETREKKEEESR 92 EELQRQYQQCQGRCQEQQQ-GQREQQQCQRKCWEQY-K-EQERG-E-HENYHNHK----K 129

EREEEQQEQHEEQDENPYIFEEDKDFETRVETEGGRIRVLKKFTEKSKLLQGIENFRLAI 152

--RN-NPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAM

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                                                                                                            This sequence represents a fovel sucrose binding protein, SBP1 isolated CC from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a CC modified amino acid sequence compared to a corresponding wild-type SBP, CC and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. CC The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing cseeds. Enhanced sucrose uptake activity in developing seeds may be considered to increase the carrobhydrate content of the seed (e.g. where the seed is the primary plant material harvested, content as soybean). In contrast, decreased sucrose uptake activity in seeds in the bedsirable where the vegetative material of the plant is capacity for the seed. The SBP regulatory regions confer specific or enhanced expression in developing wheels and so may be used to express any
       Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1998;
21-MAY-1998;
22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W90339
W90339;
                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds Disclosure; Page 34-36; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIW ) UNIV WASHINGTON STATE RES FOUND Chao WS, Grimes HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max. WO9853086-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G. max SBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified plant sucrose binding proteins - used to develop
                                                                                                  transgene in developing seeds.
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Local Similarity 33.2%; les 147; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΧH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFVSPRHFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDENEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDDEKSWLQRLNLMLTFTNTTQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSRSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381
                                                                               524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U10465.
US-047568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
       Score 702; DB 1;
Pred. No. 6.39e-49;
136; Mismatches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
         120;
                                          Length 524;
         Indels 40;
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Claim 7; Page 36-37; SBpp; English.

CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC seeds might be desirable uptake activity in developing in the seed is the primary plant material harvested,
CC seeds might be desirable uptake activity in developing seeds may be
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                       seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON STATE RES FOUND Chao WS, Grimes HD; WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max. WO9853086-A1.
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SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 15.
W90340 standard; protein; 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1999
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21-MAY-1998; U10465.
22-MAY-1997; US-047568.
          130
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                                                                                                                                         79
                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                           Local Similarity
          NRSEEEEGQQ--RN-NPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAM 186
                                                                                                                                                                            EEEDPELVTCKHQCQQQQQYTEGDKRVCLQSC-DRYHRMKQEREKQIQEETREKKEEESR 92
                                                EREEEQQEQHEEQDENPYIFEEDKDFETRVETEGGRIRVLKKFTEKSKLLQGIENFRLAI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDNQEKLTIAVLALPVN-S-PGKYELFFPAGNNKPESYYGAFSYEVLETVFNTQREKLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFD-Q--QN--EG--SIFRISR-EQVRALAPTKKSSWWPFGGESKPQFNIFSKRPTISNG
                                                                                                                                      EELQRQYQQCQGRCQEQQQ-GQREQQQCQRKCWEQY-K-EQERG-E-HENYHNHK----K 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPLNAVAFGLNAQNNQRIFLAGR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENLLMICFEVNARDNKKFTFAGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHMS--SRSSHS-KHDKS-----S---P-S-YHRISSDLKPGMVFVVPPGHPFVTIASNK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGRFFEACPEDFSQ--FQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGRLTEVGPDDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVIDGRGHLQISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILEEQRGQKRQQGQQGMFRKAKPEQIRAISQQATSPRHR-GGE-RLAINLLSQSPVYSNQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGSTVYVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQVKAPLSPGDVFVAPAGHAVTFFASKD 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQAALQTPKGKLEN
                                                                                                                                                                                                                                                                                                                                                                                                               444 AA;
                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                         114; Mismatches
                                                                                                                                                                                                                                                                                                        Score 680; DB 1;
Pred. No. 5.41e-47;
                                                                                                                                                                                                                                                                         104;
                                                                                                                                                                                                                                                                                                                                       Length 444;
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                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272
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                                                                                                     PHMSSRSSHSKH 396
                                                                VFD-Q--QN--EG--SIFRISR-EQVRALAPTKKSSWWPFGGESKPQFNIFSKRPTISNG
PHLS-RQSQGSQ 431
                                                   ILEEQRGQKRQQGQGMFRKAKPEQIRAISQQATSPRHR-GGE-RLAINLLSQSPVYSNQ
                                       384
                                                   362
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Search completed: Sat May 13 08:27:24 2000 Job time: 23 secs.